

GenCore version 4.5
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OM protein - protein search, using sw model

```
Run on:      August 14, 2001, 14:37:58 ; Search time 40.49 Seconds
              (without alignments)
              1421.405 Million cell updates/sec
```

Title:	PCT-US01-18568A-2
Perfect score:	2342
Sequence:	1 MDPDSQDPLNSLDVAKPLRKP.....VYTKVSAYLNMIIYNVMAEL 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 425026 seqs, 13205027 residues

Total number of hits satisfying chosen parameters: 425026

```
Minimum PB seq length: 0
Maximum PB seq length: 2000000000
```

```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
SPREMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_invertebrate:*
14: sp_virus:*
```

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	2337		99.8	437		09NR84	U9nr84 homo sapien
	2	2198		93.9	423		09NZAS	Q9nzas homo sapien
	3	686.5		29.3	767	13	09DGR2	Q9dgr2 xenopus lae
	4	628.5		26.8	445	11	09ER03	Q9er03 mus musculi
	5	574		24.5	457	4	09H3S3	Q9h3s3 homo sapien
	6	568.5		24.3	311	11	09ER04	Q9er04 mus musculi
	7	568		24.3	418	4	060235	060235 homo sapien
	8	562		24.0	273	11	09ER02	Q9er02 mus musculi
	9	527		22.5	279	11	09G274	Q9g274 rattus norv
	10	504.5		21.5	329	6	09GL10	Q9gl10 ovnis aries
	11	504.5		21.5	1524	13	091674	091674 xenopus lae
	12	503.5		21.5	305	11	09JHJ7	Q9jhj7 mus musculi
	13	498.5		21.3	377		P79343	P79343 bos taurus
	14	496		21.2	643	6	097506	Q97506 sus scrofa
	15	493.5		21.1	421	11	060491	060491 cavia porce
	16	488.5		20.9	1113	11	092319	Q92319 mus musculi
	17	488		20.8	812	11	09R0W3	Q9r0w3 rattus norv
	18	486		20.8	389	13	09PYX7	U9pyx7 xenopus lae
	19	484		20.7	1042	4	09Y505	Q9y505 homo sapien

20	48.3	20.6	121	4	Q9UBH2	Q9UBH2	homo sapien
21	479.5	20.5	845	13	Q9DKR1	Q9DKR1	xenopus lae
22	479	20.5	321	4	Q9NR08	Q9NR08	homo sapien
23	47H.5	20.4	6	Q29015	Q29015	sus scrofa	
24	478	20.4	314	4	Q9Y6M0	Q9Y6M0	homo sapien
25	477	20.4	1379	5	Q9V4M6	Q9V4M6	drosophila
26	476.5	20.3	311	11	Q9QUL7	Q9QUL7	mus musculus
27	476	20.3	581	5	Q9XZM7	Q9XZM7	strongyloce
28	475	20.3	422	4	Q9UL52	Q9UL52	homo sapien
29	474	20.2	855	11	Q9J117	Q9J117	rattus norv
30	473.5	20.2	260	13	Q9M7P9	Q9M7P9	paralichthy
31	473.5	20.2	310	11	Q9QY29	Q9QY29	mus musculus
32	472.5	20.2	317	4	Q9GZM4	Q9GZM4	homo sapien
33	472	20.2	312	4	Q9NS34	Q9NS34	homo sapien
34	469	20.0	321	4	Q9NR82	Q9NR82	homo sapien
35	467	19.9	855	4	Q9H350	Q9H350	homo sapien
36	464	19.8	266	13	Q9W7U0	Q9W7U0	paralichthy
37	463	19.8	855	4	Q9HCA3	Q9HCA3	homo sapien
38	459.5	19.6	342	11	Q9ES87	Q9ES87	rattus norv
39	459.5	19.6	342	11	Q9EB01	Q9EB01	rattus norv
40	459.5	19.6	1322	5	Q9NAT0	Q9NAT0	anopheles g
41	457.5	19.5	571	4	Q9Y4Y5	Q9Y4Y5	homo sapien
42	456.5	19.5	1322	5	Q9NJ55	Q9NJ55	anopheles g
43	456	19.4	868	5	Q9Y1V3	Q9Y1V3	polychaeta
44	454.5	19.4	256	5	Q9XYV1	Q9XYV1	thryoperthe
45	452.5	19.3	339	11	Q9ESD1	Q9ESD1	mus musculus

AL. COMMENTS

RESULT	ID	PRELIMINARY	PRT	437 AA
09NRS4	09NRS4			
AC	09NRS4			
DT	01-OCT-2000 (TREMUR-rel. 15, Created)			
DT	01-OCT-2000 (TREMUR-rel. 15, Last sequence update)			
DT	01-MAR-2001 (TREMUR-rel. 16, Last annotation update)			
DE	TRANSMEHRANE SERINE PROTEASE 3.			
GN	TPRSS3.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eulalia; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID 9606;			
RN	11			
RP	SEQUENCE FROM N.A.			
RC	TISSUE: PANCREATIC CARCINOMA;			
RX	MEDLINE-20283276; PubMed-10825129;			
RA	Wallrapp C., Hainel S., Muller-Pillasch F., Burghardt B., Iwamura T.,			
RA	Kutheburger M., Lerch M.M., Adler G., Gress T.M.;			
RT	* A novel transmembrane serine protease (TPRSS3) overexpressed in			
RT	pancreatic cancer.*;			
RL	Cancer Res. 60:2602-2606(2000).			
CC	-1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).			
DR	EMBL: AF179224; AAF74526.1; -			
DR	InterPro: IPR001254; -			
DR	InterPro: IPR001314; -			
DR	InterPro: IPR002172; -			
DR	Pfam: PF00057; Id1_recept_a; 1.			
DR	Pfam: PF00089; trypsin; 1.			
DR	PRINTS: PR00722; CHYMOTRYPSIN.			
DR	PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.			
DR	PROSITE: PS00135; TRYPSIN_SER; 1.			
DR	SMART: SM00192; ID1a; 1.			
SW	Protease.			
FM	SEQUENCE 437 AA; 48204 MW; 351BZPDA8657B12 CRC64;			
Query Match	99.8%; Score 2337; DB 4; Length 437;			
Best Local Similarity	100.0%; Prod. No. 72e-411;			
Matches 434;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

Wed Aug 15 07:24:53 2001

pct-us01-18568a-2.rspt

Page 2

Db	4	DPSDDPLNSLOVKPRLRPRRLPMETFRKVCIPILIALCLSLASTIIYVVLKVIIDKXYFL	63
Qy	62	CGQPLHFIPIRKOLCGELDCPLGEDEEHCVKSPFEGPAVAVRLSKDRSTLQYLDATGTM	122
Db	64	CGQPLHFIPIRKOLCGELDCPLGEDEEHCVKSPFEGPAVAVRLSKDRSTLQYLDATGTM	122
Qy	122	FSACFDFNFIIEALAEYACNCKMTSSKPTFRHVEIGPDODLDVEITENSOLRMRSSGPC	18
Db	124	FSACFDFNFIIEALAEYACNCKMTSSKPTFRHVEIGPDODLDVEITENSOLRMRSSGPC	18
Qy	182	LSGSLVSLICLACGKSLTPTPRVYGGEEASVDSMPQVSIYDOKHVCGSIIDPMHVLTA	24
Db	184	LSGSLVSLICLACGKSLTPTPRVYGGEEASVDSMPQVSIYDOKHVCGSIIDPMHVLTA	24
Qy	242	AHCFRKHDTVFWMKKYRACSDKLSGFSPLAIAKIIIEFNPMPIPKDIDLAKMLQZPLTFS	30
Db	244	AHCFRKHDTVFWMKKYRACSDKLSGFSPLAIAKIIIEFNPMPIPKDIDLAKMLQZPLTFS	30
Qy	302	GTVRPIICLDFPEDEELTPATPLMIIGMGFTKONGKNSDILLQASVOYIDSTRCNADDDYO	36
Db	304	GTVRPIICLDFPEDEELTPATPLMIIGMGFTKONGKNSDILLQASVOYIDSTRCNADDDYO	36
Qy	362	GEYTEKMKACGIPGCGVDTCCGSDSGPLMYOSDOMHNVGIVSNMGYCCGGPSTPGVYTKVS	42
Db	364	GEYTEKMKACGIPGCGVDTCCGSDSGPLMYOSDOMHNVGIVSNMGYCCGGPSTPGVYTKVS	42
Qy	422	AYLNMIIYNVMAEL	435
Db	424	AYLNMIIYNVMAEL	437

RESULT	2	
ID	099KAS	
AC	GENZAS	PRELIMINARY;
DT	01-OCT-2000 (TREMblrel. 15, Created)	PRT; 423 AA.
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)	
DT	01-MAR-2001 (TREMblrel. 16, Last annotation update)	
DE	TYPE II MEMBRANE SERINE PROTEASE.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
OX	NCBI_TaxId=9606	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Smeeleens S.S., Lorimer D.D., Wang B., Hou J., Linnevers C.;	
RT	WT-SP2, a novel type II membrane serine protease expressed in	
RT	trachea, colon, and small intestine: identification, cloning, and	
RL	chromosomal localization.	
CC	Submitted (DEC-1999) TO CHROMOSOME SERINE PROTEASE FAMILY (S1).	
DR	EMBL; AF216312; AAF31436.1; -	
DR	InterPro: IPR001234; -	
DR	InterPro: IPR001314; -	
DR	InterPro: IPR002172; -	
DR	Pfam: PFO0057; Id1_recept_a; 1.	
DR	Pfam: PFO0089; TRYPSIN; 1.	
DR	PRINTS: PR00722; CHYMOTRYPSIN.	
DR	PROSITE: PS00135; TRYPSIN_HIS; UNKNOWN_1.	
DR	PROSITE: PS00135; TRYPSIN_SER; 1.	
DR	SMART; SM00192; LDIa; 1.	
SC	Protease.	
	423 AA; 46397 MW; 90792AF0F8AFEA30 CRC64;	

```

Query Match      93.9%   Score 2198; DB 4; Length 423;
Local Similarity 97.8%   Pred. No. 7,6618;
Conservative     0; Mismatches 11; Indels 0; Caps 0

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QY	76	DGELIDCPLGDEBHCYKSPFEGBPAAVAALSKDSTLOVDLSATGNNFSCFONFEALAE	133
DB	64	DGELIDCPLGDEBHCYKSPFEGBPAAVAALSKDSTLOVDLSATGNNFSCFONFEALAE	123
QY	136	TACHOKYCSKPTFAVEIIGPDOLDVYEITENSQELRMHNSGPCLSLSVLSHLACAG	193
DB	124	TACHOKYCSKPTFAVEIIGPDOLDVYEITENSQELRMHNSGPCLSLSVLSHLACAG	183
QY	196	KSJLTPFVVOGEEASVDSMPQVSIJOYDKQHYCGSILDPJHVIYVAALCFKRNHTVFNMK	255
DB	184	KSJLTPFVVOGEEASVDSMPQVSIJOYDKQHYCGSILDPJHVIYVAALCFKRNHTVFNMK	243
QY	256	VRAOSKLGSPFLAAAKIIIEENPMYPRKNDIALMKLOPLTSGTGATPCLDPFDEE	313
DB	244	VRAOSKLGSPFLAAAKIIIEENPMYPRKNDIALMKLOPLTSGTGATPCLDPFDEE	303
QY	316	LTPATPLMIIGMGFTKQNGKMSDILLQASVOYIDSTRCNADDAVQGEVTEKMKACIPE	375
DB	304	LTPATPLMIIGMGFTKQNGKMSDILLQASVOYIDSTRCNADDAVQGEVTEKMKACIPE	363
QY	376	GGVOTCGGDSGGFLMYQSPQMHVVOIVSMGCGCGSPCTPVYTKVATYLMYIYNNMKEL	433
DB	364	GGVOTCGGDSGGFLMYQSPQMHVVOIVSMGCGCGSPCTPVYTKVATYLMYIYNNMKEL	423

RESULT	3		
09DGR2			
ID	09DGR2	PRELIMINARY:	PRT: 767 AA.
AC	09DGR2;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	EMBRYONIC SERINE PROTEASE-2.		
CN	XESP-2.		
OS	Xenopus laevis (African clawed frog).		
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC	Xenopodidae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-20363741; PubMed-10901452;		
RA	Yamada K., Takahata T., Takeshima K.;		
RT	"Isolation and characterization of three novel serine protease genes		
RT	from Xenopus laevis."		
RL	Gene 252:209-216(2000).		
DR	EMBL: AB038497; BAB08217.1; .		
KW	Protease.		
SO	SEQUENCE	767 AA;	86001 MW; E0566A387960E96E CIRC64;

[illegible]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2001, 14:39:05 ; Search time 34.69 Seconds

(Without alignments)
510.297 Million cell updates/sec

Title: PCT-US01-18568a-9

Perfect score: 1600
Sequence: 1 MDSKSSQKSRLLLLVSN.....LNIYVWKAELSRHHHHH 292

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_0601:*
1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT:*
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8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT:*
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20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1266	79.1	432	21	AAV99417
2	1266	79.1	432	22	AAAB7581
3	1266	79.1	432	22	AAAB6156
4	1266	79.1	435	20	AAV06437
5	1266	79.1	435	22	AAV72558
6	1264	79.0	233	18	AAW22986
7	1253	78.3	492	22	AAV72559
8	1230	76.9	240	21	AAAB23166
9	754.5	47.2	315	22	AAAB73465
10	746	46.6	328	21	AAAB35480
11	746	46.6	328	22	AAAB7540

12	740.5	46.3	327	22	AAV72891	PFER-C-E-HIS fusion
13	672.5	42.0	289	21	AAAB36483	Fusion gene with h
14	672.5	42.0	289	22	AAAB7543	Amino acid sequenc
15	645	40.3	288	22	AAAB36482	Fusion gene with h
16	645	40.3	288	22	AAAB7544	Amino acid sequenc
17	601.5	37.6	306	22	AAAB7544	Amino acid sequenc
18	593	37.1	319	21	AAAB36481	Fusion gene with h
19	593	37.1	319	22	AAAB7541	Amino acid sequenc
20	574	35.9	284	22	AAAB7545	Amino acid sequenc
21	528	33.0	296	21	AAV72108	Human serine prote
22	528	33.0	296	21	AAV72092	Human serine prote
23	526.5	32.9	418	17	AAAB89435	Trypsin-like enzym
24	526.5	32.9	418	20	AAV29501	Human lung tumour
25	526.5	32.9	418	20	AAV29502	Human lung tumour
26	526.5	32.9	418	20	AAV29502	Human lung tumour
27	526.5	32.9	418	21	AAV44438	Human lung tumour
28	524.5	32.8	418	20	AAV29498	Human lung tumour
29	524.5	32.8	418	21	AAV44438	Human lung tumour
30	522.5	32.7	232	17	AAAB89430	Trypsin-like enzym
31	517	32.3	273	21	AAAB1656	Mouse serine prote
32	517	32.3	311	21	AAAB1657	Mouse serine prote
33	517	32.3	445	21	AAAB1698	Mouse serine prote
34	515	32.2	238	21	AAAB1695	Mouse serine prote
35	509.5	31.8	248	21	AAAB3572	Human cancer assoc
36	509.5	31.8	327	21	AAV72093	Human cancer assoc
37	508	31.8	432	21	AAAB36901	Human TMPRSS2 prot
38	508	31.8	432	21	AAV57280	Human TMPRSS2 prot
39	507	31.7	452	20	AAV41694	Human PRO382 prote
40	507	31.7	453	21	AAAB44250	Human PRO382 (UNC3
41	507	31.7	454	21	AAAB32246	Tumour associated
42	506	31.6	432	21	AAV92050	Human PRO382 (UNC3
43	506	31.6	432	21	AAV77726	Human PRO382 (UNC3
44	506	31.6	432	21	AAV44406	Human PRO382 (UNC3
45	497	31.1	283	21	AAV81492	Human prostate-ass

ALIGNMENTS

RESULT 1	AAV99417	standard: Protein: 432 AA.
ID	AAV99417	
AC	AAV99417	
DT	08-AUG-2000	(first entry)
XX		
DE	Human PRO1570 (UNC776) amino acid sequence SEQ ID NO:275.	
XX		
KW	Human: PRO polypeptide; membrane bound protein; receptor; diagnosis;	
KW	transmembrane; secretion; immunoadhesion; pharmaceutical; screening.	
XX		
OS	Human sapiens.	
XX		
PN	MO200012708-A2.	
XX		
PD	09-MAR-2000.	
XX		
PE	01-SEP-1999.	99MO-US20111.
XX		
PR	01-SEP-1998.	98US-0098716.
PR	01-SEP-1998.	98US-0098749.
PR	01-SEP-1998.	98US-0098750.
PR	02-SEP-1998.	98US-0098803.
PR	02-SEP-1998.	98US-0098821.
PR	02-SEP-1998.	98US-0098843.
PR	09-SEP-1998.	98US-0099536.
PR	09-SEP-1998.	98US-0099596.
PR	09-SEP-1998.	98US-0099598.
PR	09-SEP-1998.	98US-0099602.
PR	10-SEP-1998.	98US-0099642.
PR	10-SEP-1998.	98US-0099741.
PR	10-SEP-1998.	98US-0099754.

Db 259 kigsfslavakllllefmpykndialmkqlfplrtsgvtrpicipfideelpatp 318
 Oy 171 LMIIGGFTKQNGKMSDILLOASVOVISTRCNADDAVQGEVTEKMCAGIPEGCVDTG 230
 Db 319 lwllygftckqngkmsdilllqasvqldstrcnaddaygvevtekmccaglpegvdtc 378
 Oy 231 OGDGSGPLMTQSDQMHVGVIVSWGCGGSPSTPGVYTKYSATLNMVYNNWKAEL 284
 Db 379 qgdsqgplmyqsdqwhvvgivswgycgspstpgvlytkvsaylnvlynnwkael 432

RESULT 2

AAB87581
 ID AAB87581 standard; Protein: 432 AA.

AC AAB87581;

DT 15-MAY-2001 (first entry)

DE Human PRO1570.

XX Human; PRO protein; mapping.

OS Homo sapiens.

XX MO200116318-A2.

XX 08-MAR-2001.

XX 24-AUG-2000; 2000MO-US23328.

XX 01-SEP-1999; 99MO-US20111.

XX 15-SEP-1999; 99MO-US21090.

XX 07-DEC-1999; 99US-0169495.

XX 09-DEC-1999; 99US-0170262.

XX 11-JAN-2000; 2000US-0175481.

XX 18-FEB-2000; 2000MO-US04341.

XX 18-FEB-2000; 2000MO-US04342.

XX 22-FEB-2000; 2000MO-US04414.

XX 01-MAR-2000; 2000MO-US05601.

XX 03-MAR-2000; 2000US-0187202.

XX 25-APR-2000; 2000US-0199397.

XX 22-MAY-2000; 2000MO-US14042.

XX 05-JUN-2000; 2000US-0209832.

XX (GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

XX MPI: 2001-183260/18.

XX N-PSDB: AAF92113.

XX Eighty four nucleic acids encoding PRO polypeptides, useful in

XX molecular biology, including use as hybridization probes, and in

XX PT chromosome. and gene mapping.

XX Claim 12: Fig 112: 278bp; English.

XX The present sequence is a human PRO polypeptide (secreted and

XX transmembrane). The PRO protein, and PRO agonists, PRO antagonists or

XX anti-PRO antibodies are useful for preparation of a medicament useful in

XX the treatment of a condition which is responsive to the PRO protein.

XX CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be

XX employed as molecular weight markers for protein electrophoresis. The PRO

XX coding sequence has applications in molecular biology, including use as

XX hybridisation probes, and in chromosome and gene mapping.

XX Sequence 432 AA;

XX Query Match 79.1%; Score 1266; DB 22; Length 432;

XX Best Local Similarity 97.4%; Pred. No. 1.9e-112;

Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 51 KIVGCTALVDSPMPOVSIQYDKQNVGCSILDIHIVLTAAHCFKHTTVFMKKVACSD 110
 Db 199 rvyggeeasvdsprvgslyqydkqvcgsslldphvltcaahcfhrhtvfmkvragsd 258
 Oy 111 KLSFPSLAVALKIIIEFNPMPYKNDIALMKLQPLRTSGVTRPICLFPFDEELPATP 170
 Db 259 kigsfslavakllllefmpykndialmkqlfplrtsgvtrpicipfideelpatp 318
 Oy 171 LMIIGGFTKQNGKMSDILLOASVOVISTRCNADDAVQGEVTEKMCAGIPEGCVDTG 230
 Db 319 lwllygftckqngkmsdilllqasvqldstrcnaddaygvevtekmccaglpegvdtc 378
 Oy 231 OGDGSGPLMTQSDQMHVGVIVSWGCGGSPSTPGVYTKYSATLNMVYNNWKAEL 284
 Db 379 qgdsqgplmyqsdqwhvvgivswgycgspstpgvlytkvsaylnvlynnwkael 432

RESULT 3

AAB66166
 ID AAB66166 standard; Protein: 432 AA.

AC AAB66166;

DT 02-APR-2001 (first entry)

DE Protein of the invention #78.

XX Secreted; transmembrane; gene therapy.

XX Unidentified.

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XX (GETH) GENENTECH INC.

XX Baker KP, Bolstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

XX Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

XX Pan J, Paout NF, Roy MA, Smith V, Stewart TA, Tumas D;

XX Watanabe CK, Williams PM, Wood WI;

XX MPI: 2001-071395/08.

XX Secreted and transmembrane proteins and nucleic acids designated PRO,

XX useful as hybridization probes, in chromosome and gene mapping and gene

XX therapy -

XX Claim 1: Fig 156: 787bp; English.

XX The present invention relates to secreted and transmembrane proteins.

XX These proteins and the DNA encoding them may be used as hybridization

XX probes, in chromosome and gene mapping and in the generation of

XX anti-sense RNA and DNA. They may also be used to generate either

XX transgenic animals or knockout animals which are in turn useful for

XX development and screening of therapeutically useful reagents.

XX The nucleic acids may also be used in gene therapy.